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0 679 716 A1

⑫

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⑲ Applicant: **Matsubara, Kenichi**
Room 804, 18-1, Yamadahl-gashi 3-chome
Suita-shi,
Osaka 565 (JP)
Applicant: **Okubo, Kousaku**
11-26, Segawa 2-chome
Minoo-shi,
Osaka 562 (JP)

⑳ Inventor: **Matsubara, Kenichi**
Room 804, 18-1, Yamadahl-gashi 3-chome
Suita-shi,
Osaka 565 (JP)
Inventor: **Okubo, Kousaku**
11-26, Segawa 2-chome
Minoo-shi,
Osaka 562 (JP)

㉑ Representative: **Vossius, Tilman et al**
Dr. Volker Vossius,
Patent- und Rechtsanwaltskanzlei,
Holbeinstraße 5
D-81679 München (DE)

㉒ **GENE SIGNATURE**

㉓ A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomoly or discriminating cells. The cloned gene can produce proteins utilizable as a medicine or the like.

EP 0 679 716 A1

Table 1

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AO	AS	AU	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
95	00106	00094	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
96	00107	00095	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
97	00108	00096	31	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
98	00109	00097	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
99	00110	00098	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
100	00111	00099	38	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
101	00113	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
102	00114	00101	38	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
103	00115	00102	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
104	00116	00103	17	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
105	00117	00104	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
106	00118	00105	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
108	00120	00107	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
109	00121	00108	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
110	00122	00109	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
111	00123	00110	14	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
112	00124	00111	6	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
113	00125	00112	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
114	00127	00113	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
115	00128	00114	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
116	00129	00115	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
117	00130	00116	24	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
118	00131	00117	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
119	00132	00118	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
120	00133	00119	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
121	00134	00120	24	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
122	00135	00121	61	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
123	00136	00122	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
124	00137	00123	16	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
125	00138	00124	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
126	00139	00125	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
127	00140	00126	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
128	00141	00127	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
129	00142	00128	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:

- (A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
- (B) STREET: 41-8, Takada 3-chrome, Toshima-ku
- (C) CITY: Tokyo
- 10 (E) COUNTRY: JAPAN
- (F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

15 (iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
- (B) COMPUTER: IBM PC compatible
- 20 (C) OPERATING SYSTEM: PC-DOS/ MS-DOS
- (D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

- (A) APPLICATION NUMBER: EP 95900295.7

25 (vi) PRIOR APPLICATION DATA

- (A) APPLICATION NUMBER: PCT/JP94/01916
- (B) FILING DATE: 11. November 1994

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5 SEQ ID NO:111
 SEQUENCE LENGTH:375
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00124
 SEQUENCE DESCRIPTION:
 GATCCTACCT ATCAAGCACT AAAAAAGTGA ACCATTATAC TTTATATCTG TAATGATACT 60
 GATTATGAAA TGTCCCCCTCA AACTCATTGC AGCAGATAAC TTTTTGAGT CATTGACTTC 120
 ATTTTATATT TAAAAAAATTA TGGAATATCA TCTGTCTTA TATTCTANTT AANGTTGTGC 180
 ATAATGCTTT GGAANAATGG GTCTTTATA GGAAAAAAACC TGGGATAACT GATTCTATG 240
 GCTTCAGAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTT 300
 ACTGTCAGNT TAANTTACAG CTTTATGGG TGGTTAACCTT TTCTGTNCATT TTCAAAAAAN 360
 CCNGGGGNNN NNNNN 375

10 SEQ ID NO:112
 SEQUENCE LENGTH:356
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00125
 SEQUENCE DESCRIPTION:
 GATCTCTGTT TTGTTGTTGA AAATTCAATT GTATACTTT GTTTNATCT AGGACTTCAT 60
 GTTTTTNAAG CACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120
 AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180
 TATGANTTAA GCTGTAAGGC CTGAGCTCT GTGTGATAAC TTTCTTTTCAAATTATAG 240
 TTTATCTNCT GTATAACTGA TTTATAAAGG TTTTGTAACA TTTNTNAATA CTCATTGTCA 300
 ATTTGAGAAA AAGGACATAT GAGTTTTNC ATTTATTAAT GNAACTNCCT TTGAAA 356

15 SEQ ID NO:113
 SEQUENCE LENGTH:351
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00127
 SEQUENCE DESCRIPTION:
 GATCACATTA TNATAAATAA ATGAAAAAAAT GATTAATCT GTAATAAACT GGTTTATTGT 60
 GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTA CTCTGCCTCA CAAACACAT 120
 GCTAGGATAT AACCCCCAAA ATAAGTATT AACTTGCAT TAGGTATAAA GGAGACTGGG 180
 TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240
 TTCTGTAATT GAGAAAATGT TCACCAAATN ATACTTTTA GTGATTACA TGTACATTTT 300
 ATAGGGACA TGTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

20 SEQ ID NO:114
 SEQUENCE LENGTH:352
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00128

5 SEQ ID NO:7844
 SEQUENCE LENGTH:37
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTCGCTGCC CATCCTATA CAGGCTCAGT TTTGTCT 37

10 SEQ ID NO:7845
 SEQUENCE LENGTH:37
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTCGCTGCC CATGTATAGG GACAGCATT CTGAGAG 37

20 SEQ ID NO:7846
 SEQUENCE LENGTH:38
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

30 SEQ ID NO:7847
 SEQUENCE LENGTH:22
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 CCAGGGTTTT CCCAGTCACG AC 22

40 SEQ ID NO:7848
 SEQUENCE LENGTH:22
 SEQUENCE TYPE:nucleic acid
 STRANDEDNESS:single
 TOPOLOGY:linear
 SEQUENCE DESCRIPTION:
 TCACACAGGA AACAGCTATG AC 22

50 Claims

1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed
 55 under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

5

3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

10

4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

15

20 5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

25

6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

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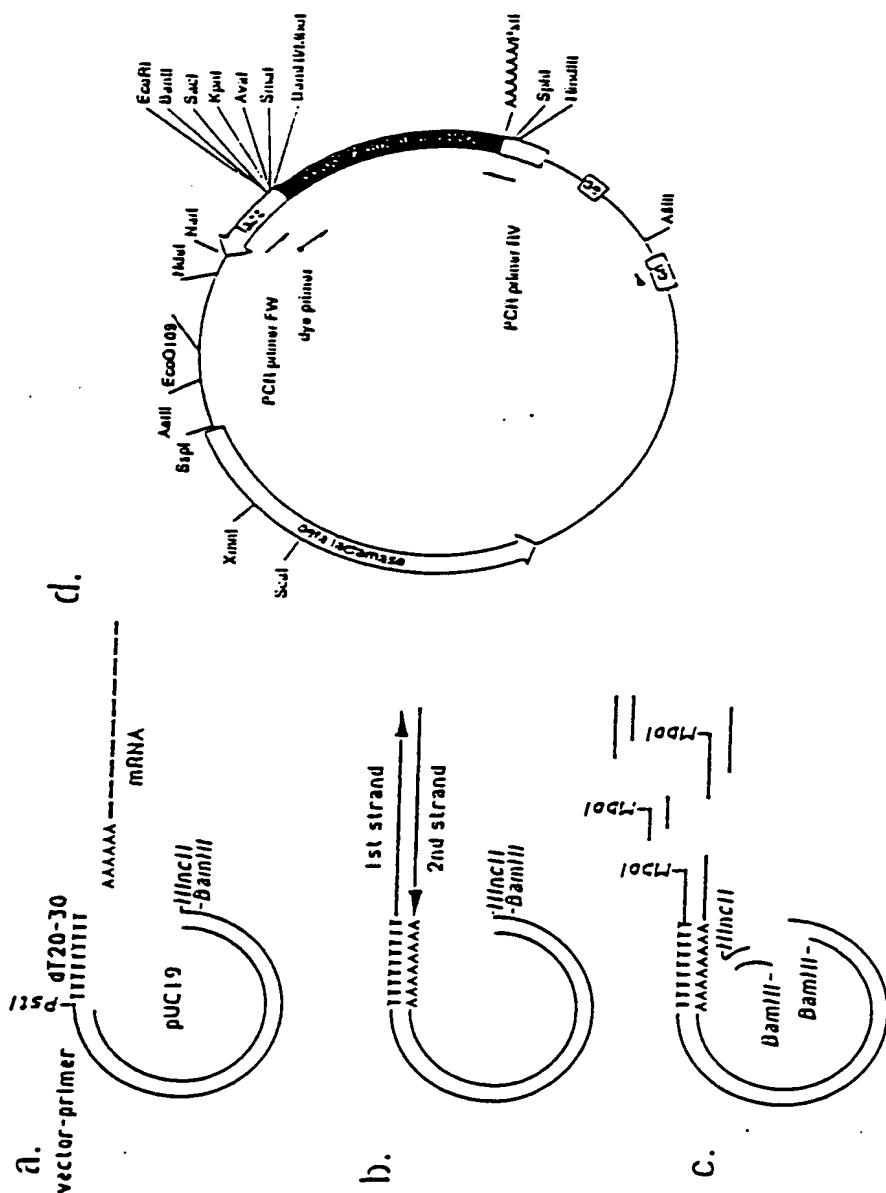
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Fig. 1



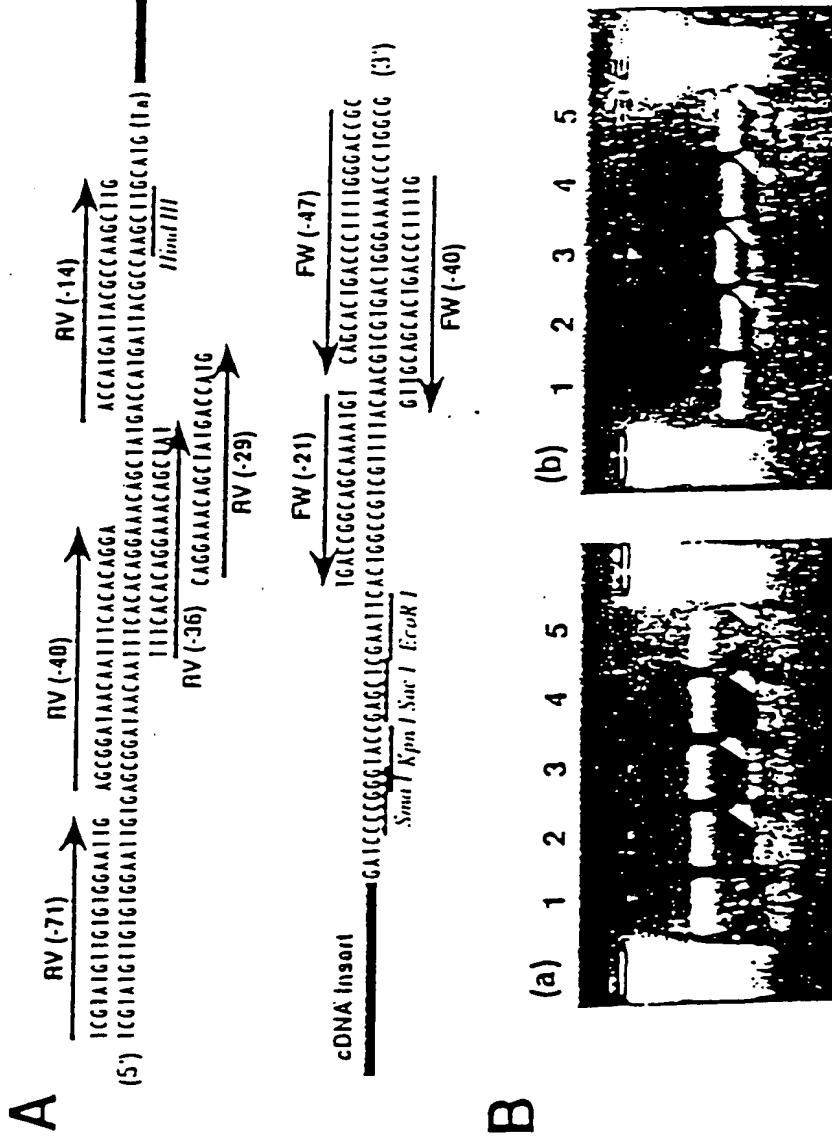


Fig. 2

Fig. 3

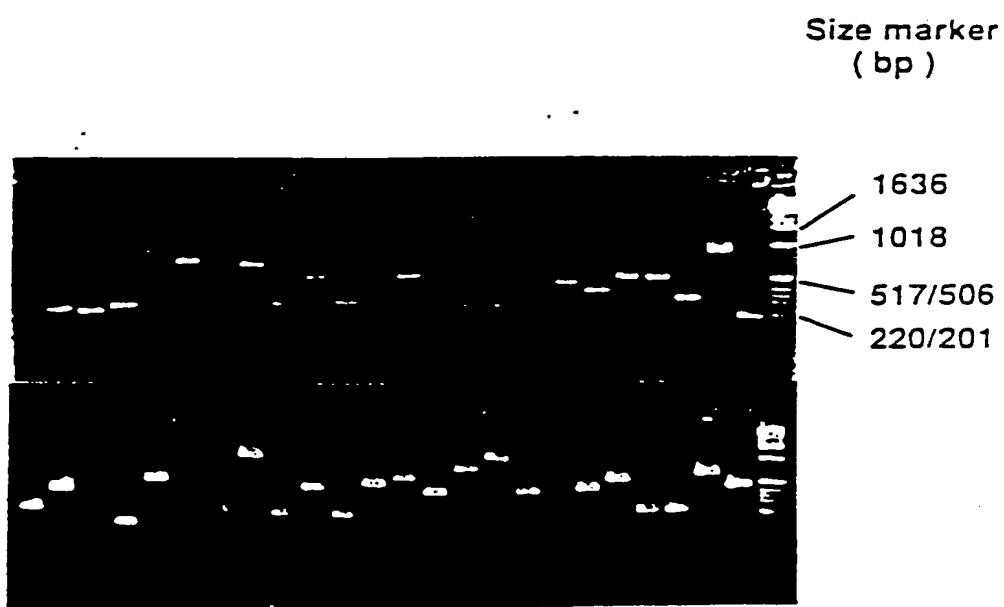


Fig. 4

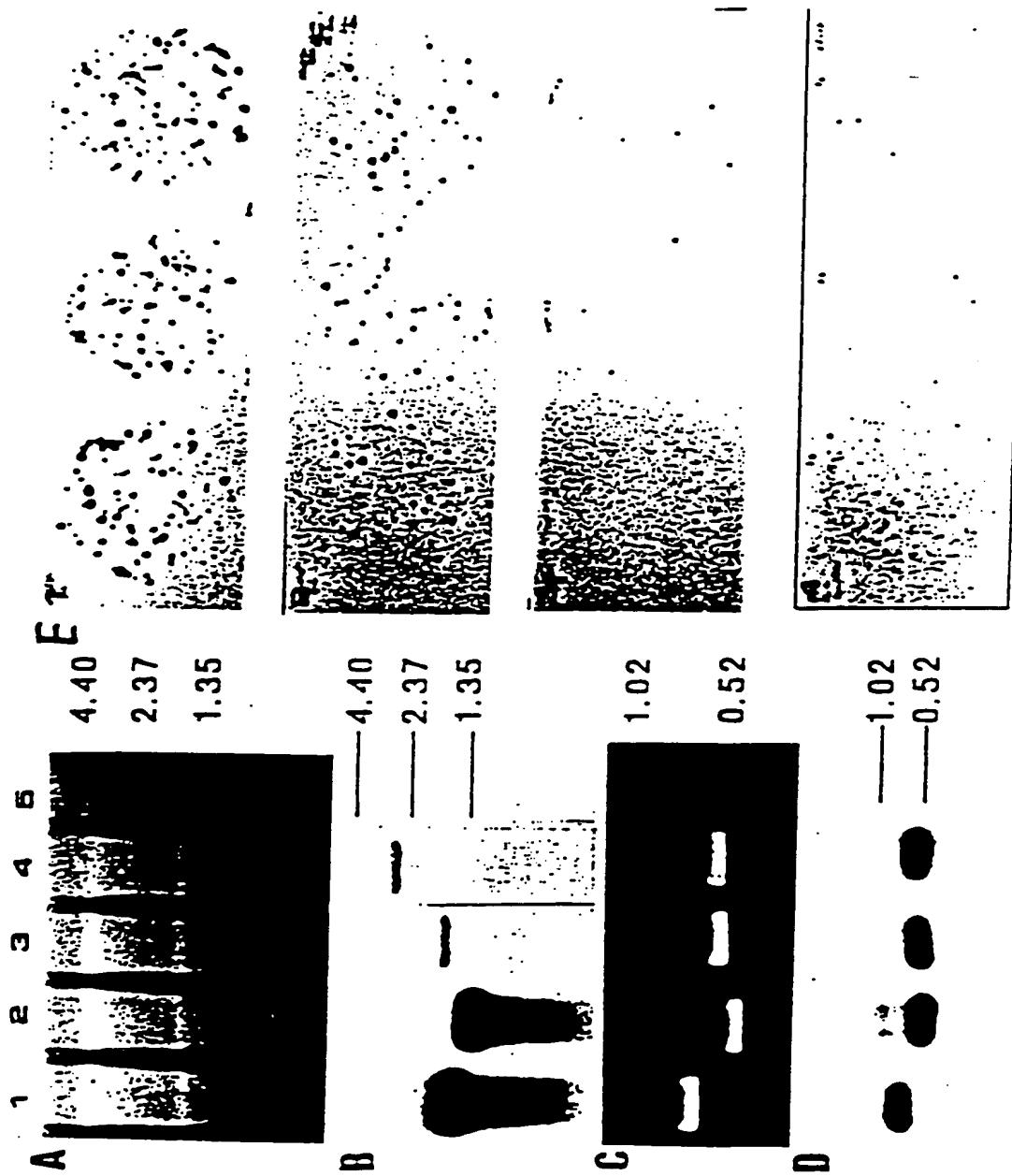


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- α	α 1-antitrypsin	HsRNP core protein A1	Inter- α -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	In 902 (%)	A "in 0,000 (%)"	B "in 0,000 (%)"	C "in 26,400 (%)"
	a15	Elongation factor - 1 α	22 (2.2)	307 (3.5)	NT	NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT	NT
	lb030	α -1-antitrypsin	0 (0.0)	119 (1.4)	NT	NT
I	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT	NT
	c13a04	NADP (H) Menadione oxidoreductase	4 (0.4)	27 (0.3)	NT	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT	NT
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT	NT
	s155	unknown	1	2	5 (0.02)	5 (0.02)
	s159	unknown	1	2	1 (0.02)	1 (0.02)
	s639	unknown	1	1	3 (0.01)	3 (0.01)
	s635	unknown	1	0	2 (0.01)	2 (0.01)
II	s170	unknown	1	0	1 (0.004)	1 (0.004)
	s154	unknown	1	0	1 (0.004)	1 (0.004)
	s167	unknown	1	0	1 (0.004)	1 (0.004)
	s615	unknown	1	0	1 (0.004)	1 (0.004)
	s617	unknown	0	0	0 (<0.001)	0 (<0.001)
	s632	unknown	0	0	0 (<0.001)	0 (<0.001)

Fig. 6

GS	CI	Chromosomal position	Sense	Antisense	AT	AT	AT	AT	AT	AT	AT	AT	AT	AT	AT	AT	AT	AT	AT	
61000700	pm1266		CAGAGCCCAGTACACAT	AAGTTTATGTTGGGTCAAG	40	114	115	104	110	110	1	2								
61001026	pm1244		ATGGGGACCTTACCTGAA	CCAGCTCTTACTTGAGAA	40	03	04	200	200	200										
61001035	pm1003		TGGACTTGATACCTACT	ACAGTACCCCTGATGGCT	40	124	124	101	107	107										
61001067	pm1172		GTCACTCTGGCTTACGAC	ACCACTTCTGGCTACACIT	50	104	104	100	100	100										
61001081	pm0347		GGCCCTAACAGGGAACTC	TAATTCACACTCCGTAAC	51	114	114	116	200	200										
61001116	pm1171		GGGTTTCAATGGGTGAGCC	GGCCCAACTCTAACACAA	49	95	95	70	107	107										
61001101	pm0669		TGGTGTGATGAACTTCTTG	GGCTGAACTTACACITCTG	47	97	97		200	200										
61001269	pm1131		TTAAAGAACCCCTTAAGGACC	AATAATCTGGTGTACITAC	47	97	98		200	200										
61001246	pm0902		TCAAGTCGGTGGGAGAG	AAC1CACAGCACAGTAATTG	51	120	122	200	200	200										
61001146	pm1150		AAGGTTCACGGATATTGCAA	TCGAAATGGCCAACTCATI	47	130	125	200	200	200										
61001164	pm1149		CCAAAGACCTCCGTGAA	TTTGGGGAGCCATAGACAG	51	100	100	200	200	200										
61001140	pm0427		TACTCAGGGAAAGATAAAC	CAGTGGACCAATTTCTTA	40	90	98		200	200										
610011521	pm1205		CCCAAATCAAATGTTAATG	TTTGGATCATAGATGAAAGT	43	102	115	100	200	200										
610011514	pm12231		CCAGAGAGTCAGGGATG	GGTAAATAGGTCAAAGATCT	46	57	57	70	155	155										
61001172	pm1204		CCAAACATGGCTCTAGACTG	AAACCTTATGGGCTCTCT	44	58	58	53	200	200										
61001120	pm1130		CATGATCTCTGGGGGTA	AAACACTAGTGGCAGCAT	46	04	109		200	200										
61001165	pm11730		AGGCTAAATGTCGGCATGT	CCCGTTATGTCACAIGCT	40	119	119	93	115	115										
610011001	pm0901		AAAGGAATACAAAATACAA	TTCATATGTTAACCGATA	40	50	50		200	200										
61001050	pm0925		TAATGTTACGCTGATAG	TAATGTTAAATGCGCTTAA	45	05	05		200	200										
610011213	pm12010		CCAGAGGAAAGGGAGCT	CGGAAATAGGAGATCAAACAG	47	125	125	150	200	200										
610011212	pm09135		TCGAGTTTCTCTCTAA	GGAAATAAIGCGCTCAGTG	42	103	103		200	200										
610011240	pm12093		AGTCCTCTGGCTCCCAT	TATGTCAGTCGCTTATG	52	117	117		200	200										
610011420	pm12435		TTTGTACCTACGTAGAGACT	ATCGGCUCCACATAGIGA	45	105	105		200	200										
61001142	pm11671		TTATAGGGAGCATATCTCTG	AGTCCTCATCTCCATG	45	67	65	200	200	200										
61001113	pm11245		TTGGCTTCCGJCCTTAAT	ATGTTACATTTGGTAACTAGT	45	75	75		150	150										
610011315	pm1210		ATCIACTGTTGTGAGAG	ACIGATTGTTGCACTCTG	44	60	62		200	200										
61000274	pm1440		CGAACATTCACCCCTATA	ATGTTTATTAGGAGGAA	43	66	63		200	200										
610011001	pm11730		TCGGCCTTTGGTGGG	GGCCCACTAGACATAGTC	45	115	115		200	200										
610011210	pm12434		AAAGGAAGAACACTGCTAA	ATGTTAGACAAATCCAAQ	42	90	90		200	200										
610011660	pm1210		GTAGTCCTCTGGCTTAC	AGGATTGTTGATTCTACAT	43	77	77		200	200										
610011726	pm11726		GGTCCTGTTATTTCACAT	AAACAGAGGATGTTGTCAGA	43	75	75		155	155										
610011022	pm11206		GATCCCTGGGGTGGTACAT	CGGCAAAATACGTTAACTAT	46	03	03		150	150										
610011414	pm12209		ACCCAGTCCTAACCTCAGT	ACAC1CCCTCAGGCTTACI	55	105	105		150	150										
610011465	pm12155		ATCAGCCTGGCTGAGTAT	TTAAAGAGATGAAATTGTTG	42	130	130		150	150										
61000271	pm11252		GTCCTTGCTCTCTGTTTA	AGGCAATTATTCGAGGTTAA	43	90	90		150	150										

Fig. 7

9100044	pm02254	GTTCAGTTTATTCAGAGCA	42	62	62	>200	69
9100132	pm1151	GICATATTCATCATCA	43	80	80	-	-
91001215	pm0980	TAGAGTCAGTGGCTGTG	43	100	100	130	-
91001390	pm2167	CATCCCATACATACAGTC	43	116	116	>200	180
91000993	pm0901	TCTGGTGAAGCAGCACAA	43	101	102	113	200
91002694	pm1809	AAGCAATGGCTATCCACAG	43	87	87	>200	200
91001065	pm02119	TCACCCAGATAATTGCTCA	44	120	120	-	-
91001101	pm2164	TTACCTTACCGTGTCTTAC	44	102	104	145	200
91001161	pm1160	ATTGTTGAGTGTGTTCATCA	43	69	69	100	200
91000351	pm22720	AAATGCAATGCTCTTCA	43	101	99	>200	200
91001226	pm1151	CATTGAAACAGCAACACAG	44	78	76	72	>200
91001234	pm1216	TAGGCAAAAACGGAAAGAG	43	138	138	>200	200
91001457	pm1785	TATATGCAAATATCCAAAGCTG	48	65	65	110	>200
91001323	pm02265	TITGTAACCGTGTGCTCAGT	46	90	90	>200	200
91001524	pm02270	GCACCTTAAGCTCCAAAGT	42	86	70	>200	100
91001567	pm2619	TCTGCAATGACAAAGGACAC	49	102	102	>200	200
91002621	pm09931	GACCTGAAAGTGTGTAAGT	43	62	62	>200	45
91001115	pm02261	AGCCAAACCTGGGGTCACT	45	119	119	>200	2
91001459	pm02219	AATCATTTGGCAAGACIGTA	56	159	159	115	>200
91001129	pm1101	TCAGGCGAGTCGCGAGATA	45	88	89	130	-
91001201	pm0956	AACGATTTGCTTGTCACTAG	44	77	76	170	-
91001124	pm2527	TTCACCTTATGGCTCTAC	47	81	81	105	70
91001240	pm1208	IGTATGGATTTGGATCTC	48	93	93	118	180
91000250	pm09935	TTGCCATCAAACACATACA	44	95	95	-	85
91001055	pm09359	TTAAGAAATCCCTCATGG	43	55	55	-	-
91001137	pm02511	AAGTATGTCAGAGATGA	44	74	74	72	73
91001264	pm12245	TGTAATATGCTATCTCTCT	45	128	128	>200	200
91002120	pm12661	AICAAACAAACAAATCCAGA	47	100	100	>200	200
91001159	pm0880	GAATAGCTGGAGATTCAC	42	117	121	124	95
91001113	pm04415	AAAGTGGCTTGAAGGACTTAC	46	100	100	84	95
91001327	pm12943	AGGGTGAAGGGTTATTCAG	50	151	151	>200	160
91001469	pm02519	AACCTCTAGTAAGGCATG	47	03	05	-	2
91002120	pm2810	CTGTAAGGTTGGATTAATGT	37	47	47	125	53
91000213	pm02566	AGTGTGGAGAGACTTGTAG	42	75	75	145	>200
91001161	pm2756	TCTCCCTATCAACCACT	48	130	130	103	>200
91001193	pm1193	CACAGCATAAAGATCTATA	49	98	98	>200	120
91001215	pm2790	CATCATGGTACAGTCAGAG	46	100	100	-	-
91001224	pm1355	AGATGCAATGCTCTCTAGG	44	83	82	01	67
91001208	pm02668	CCAAAGTGTCTAGGGTTACQ	47	97	97	>200	200
91001139	pm2645	CTAAAGATTAATGGATCC	47	95	95	>200	>200
91000114		AGTGTGGTGTGAGGAGA	46	104	104	>200	-

Fig. 8

91001044	TGTAAAGCTTAACAGAGTCA	AGACAGACTTAAGCCACATCA
91001045	GCCTCTTCGCGCGCGGGT	GGAGTTAACAGGCTATTCCTCC
91001046	ACTGAAATGGAAACATAGCT	TACATTACAGACATGIGA
91001047	TGCTAGCTTCCTCCCTTAA	GGAGCTTCTGTTGTCCTA
91001048	CATGAACTGCTACGACAA	GCTTACATTAATGCTAACCC
91001049	AATAAAATGAAATAGACAT	ATTTAGTTAACAGGAGAAAT
91001050	CTTTAAAGTTGATTGGG	CATTCACACTTACATTCCT
91001051	CGCTCTAAACCTGAAATC	AATGGCTTATTCCTCAG
91001052	ATCCAAATTACCTTATGTC	ACGAAACTTATGGAGAT
91001053	TCCCCTATCTCAGCTGAGT	TGAGAAACAAAGGAACTG
91001054	TTGGAAATGGAAACCTGCTA	ACTATGGCCCTAAATGG
91001055	CCCTTGTCTTACATGTTCA	TATTAATCTCCCTCAT
91001056	ACAGTCTAAATCAAAGGTG	TCTGACAACTCAAGGCGAT
91001057	TTTGTTGGGACTATGTAAT	TCACTTTATGGGACCA
91001058	CTCTCCATGTTCTACAAAG	TAGAGGAAACCTGGGTT
91001059	ATATCACTCTCCATCCAT	TCAATACGCTCTCAAGC
91001060	CAGAAATAAGTCAGCAAT	TCTATCTGCACTTAAAGT
91001061	AAAATCTGTTTATTCCT	GTTGATCTACGTCATTC
91001062	TAATTTGTGAAATCTCTGG	ACACATTGGGTTGCTTAAC
91001063	TGIGACAGCAGGAGCTCAT	TGTACATTTAATTCACCC
91001064	CACTCACAGCAAGGAAC	ACCTAATGCTAGAGAAAC
91001065	TGACIGCAATAAGGAGTGT	GAACATACACGGTTATTC
91001066	GCTTCAGCAGATTCAGGT	ACTTCCTGAGGACACA
91001067	TGIGITCTCCGCTTGTAG	GTTACATGGCTGGTACAG
91001068	GGATCAGACCAATAGTG	GCAAGGTAAACAGATA
91001069	GAAGCCACCTGACCCICA	GGAGAGTATGGGAAACGT
91001070	GCTACACTTGTAAAGTGT	TTAAGAAGCTTACCTGGATA
91001071	GCCCTTAAGATTACGCGC	ACCCCTGGGCTTCAGG
91001072	TGCTGGATGACTCTACACG	TCCCTATGAGGCGCTT
91001073	CTCTCGGACTAGCTGACTC	CAAAGGGCTTAAAGGACAT
91001074	TGCTAAAGTGTGAAACA	ATCTAGTCCTAACCCAGTA
91001075	GGAGCCACAGGATGATG	AAATGGCTTACAAAGA
91001076	AGCCATCTGGTTAAGCTTA	GGAGGAGAAGAACTTCAC
91001077	TCTAGGGTTTAAAGCCAG	CCACATCCTACAGGGAGT
91001078	GTCAGCTAAAGTGTGAAACA	TTATAGTGGACACAGAGT
91001079	GGAGCCACAGGATGATG	ACAATGGCTTACAAAGA
91001080	AGCCATCTGGTTAAGCTTA	AGTGGCACCACCTCCGTC
91001081	TCTAGGGTTTAAAGCCAG	AGAAAGGCCAAAGTAGCC
91001082	GTCAGCTAAAGTGTGAAACA	AAGGGGTTGAGTGGGTTCT
91001083	GGCTCTGGCTCCCACTAAAC	TTATCTGCACTACAA
91001084	TACAGGCCCCTCCAGCTAAAC	46 65 65 190 ,200 - 1
91001085		46 65 65 190 ,200 - 1
91001086		46 65 65 190 ,200 - 1
91001087		46 65 65 190 ,200 - 1
91001088		46 65 65 190 ,200 - 1
91001089		46 65 65 190 ,200 - 1
91001090		46 65 65 190 ,200 - 1
91001091		46 65 65 190 ,200 - 1
91001092		46 65 65 190 ,200 - 1
91001093		46 65 65 190 ,200 - 1
91001094		46 65 65 190 ,200 - 1
91001095		46 65 65 190 ,200 - 1
91001096		46 65 65 190 ,200 - 1
91001097		46 65 65 190 ,200 - 1
91001098		46 65 65 190 ,200 - 1
91001099		46 65 65 190 ,200 - 1
91001100		46 65 65 190 ,200 - 1
91001101		46 65 65 190 ,200 - 1
91001102		46 65 65 190 ,200 - 1
91001103		46 65 65 190 ,200 - 1
91001104		46 65 65 190 ,200 - 1
91001105		46 65 65 190 ,200 - 1
91001106		46 65 65 190 ,200 - 1
91001107		46 65 65 190 ,200 - 1
91001108		46 65 65 190 ,200 - 1
91001109		46 65 65 190 ,200 - 1
91001110		46 65 65 190 ,200 - 1
91001111		46 65 65 190 ,200 - 1
91001112		46 65 65 190 ,200 - 1
91001113		46 65 65 190 ,200 - 1
91001114		46 65 65 190 ,200 - 1
91001115		46 65 65 190 ,200 - 1
91001116		46 65 65 190 ,200 - 1
91001117		46 65 65 190 ,200 - 1
91001118		46 65 65 190 ,200 - 1
91001119		46 65 65 190 ,200 - 1
91001120		46 65 65 190 ,200 - 1
91001121		46 65 65 190 ,200 - 1
91001122		46 65 65 190 ,200 - 1
91001123		46 65 65 190 ,200 - 1
91001124		46 65 65 190 ,200 - 1
91001125		46 65 65 190 ,200 - 1
91001126		46 65 65 190 ,200 - 1
91001127		46 65 65 190 ,200 - 1
91001128		46 65 65 190 ,200 - 1
91001129		46 65 65 190 ,200 - 1
91001130		46 65 65 190 ,200 - 1
91001131		46 65 65 190 ,200 - 1
91001132		46 65 65 190 ,200 - 1
91001133		46 65 65 190 ,200 - 1
91001134		46 65 65 190 ,200 - 1
91001135		46 65 65 190 ,200 - 1
91001136		46 65 65 190 ,200 - 1
91001137		46 65 65 190 ,200 - 1
91001138		46 65 65 190 ,200 - 1
91001139		46 65 65 190 ,200 - 1
91001140		46 65 65 190 ,200 - 1
91001141		46 65 65 190 ,200 - 1
91001142		46 65 65 190 ,200 - 1
91001143		46 65 65 190 ,200 - 1
91001144		46 65 65 190 ,200 - 1
91001145		46 65 65 190 ,200 - 1
91001146		46 65 65 190 ,200 - 1
91001147		46 65 65 190 ,200 - 1
91001148		46 65 65 190 ,200 - 1
91001149		46 65 65 190 ,200 - 1
91001150		46 65 65 190 ,200 - 1
91001151		46 65 65 190 ,200 - 1
91001152		46 65 65 190 ,200 - 1
91001153		46 65 65 190 ,200 - 1
91001154		46 65 65 190 ,200 - 1
91001155		46 65 65 190 ,200 - 1
91001156		46 65 65 190 ,200 - 1
91001157		46 65 65 190 ,200 - 1
91001158		46 65 65 190 ,200 - 1
91001159		46 65 65 190 ,200 - 1
91001160		46 65 65 190 ,200 - 1
91001161		46 65 65 190 ,200 - 1
91001162		46 65 65 190 ,200 - 1
91001163		46 65 65 190 ,200 - 1
91001164		46 65 65 190 ,200 - 1
91001165		46 65 65 190 ,200 - 1
91001166		46 65 65 190 ,200 - 1
91001167		46 65 65 190 ,200 - 1
91001168		46 65 65 190 ,200 - 1
91001169		46 65 65 190 ,200 - 1
91001170		46 65 65 190 ,200 - 1
91001171		46 65 65 190 ,200 - 1
91001172		46 65 65 190 ,200 - 1
91001173		46 65 65 190 ,200 - 1
91001174		46 65 65 190 ,200 - 1
91001175		46 65 65 190 ,200 - 1
91001176		46 65 65 190 ,200 - 1
91001177		46 65 65 190 ,200 - 1
91001178		46 65 65 190 ,200 - 1
91001179		46 65 65 190 ,200 - 1
91001180		46 65 65 190 ,200 - 1
91001181		46 65 65 190 ,200 - 1
91001182		46 65 65 190 ,200 - 1
91001183		46 65 65 190 ,200 - 1
91001184		46 65 65 190 ,200 - 1
91001185		46 65 65 190 ,200 - 1
91001186		46 65 65 190 ,200 - 1
91001187		46 65 65 190 ,200 - 1
91001188		46 65 65 190 ,200 - 1
91001189		46 65 65 190 ,200 - 1
91001190		46 65 65 190 ,200 - 1
91001191		46 65 65 190 ,200 - 1
91001192		46 65 65 190 ,200 - 1
91001193		46 65 65 190 ,200 - 1
91001194		46 65 65 190 ,200 - 1
91001195		46 65 65 190 ,200 - 1
91001196		46 65 65 190 ,200 - 1
91001197		46 65 65 190 ,200 - 1
91001198		46 65 65 190 ,200 - 1
91001199		46 65 65 190 ,200 - 1
91001200		46 65 65 190 ,200 - 1

Fig. 9

91.000999	x	x	TCAACCACCACTTATTAGCA	47	103	-	-
91.001119	x	x	GGAGGGAGATAAGATGT	46	70	135	130
91.001111	x	x	TCTATAAGTGGACCAGT	46	65	65	200
91.001106	x	x	TATGGCCATGAGTGGTAA	40	65	>200	40
91.001106	x	x	ATCTCTGGCTAAATACCTG	47	62	62	2
91.001106	x	x	GTCTCCATGGAGTAAAT	46	70	70	70
91.001104	x	x	TTCGAATGACATCTAT	44	69	69	170
91.000803	x	x	TTATGATACAGGCACT	43	130	130	130
91.000803	x	x	TTACGATACAGGCACT	43	61	61	2
91.000801	x	x	ATGAGCTGGAGGAA	45	91	91	110
91.000801	x	x	AGTGTACAGGCTGAA	43	66	66	100
91.000801	x	x	TITTTATGTTGCTTCA	43	110	110	150
91.000801	x	x	TTATGTTGTTTACACGG	43	61	61	2
91.000801	x	x	ATTCCTTGTCTCAGTAA	46	82	>200	42
91.000801	x	x	CAGTCACCCACAGGTAT	49	95	95	160
91.000801	x	x	CCGTGTAGGTGAGAAAG	49	78	80	>200
91.000801	x	x	ACATTTTATTTTCAACG	37	45	45	2
91.000801	x	x	GCACACTAACATCCAACT	50	123	>200	150
91.000801	x	x	GATTTACCCATAGGAGC	50	101	101	66
91.000801	x	x	ATAGTTGGTGTGACACAA	43	80	>200	170
91.000801	x	x	ACACCCATAGGAGTTAC	47	91	91	>200
91.000801	x	x	CTCTTAAACCAACAGGAG	50	96	>200	125
91.000801	x	x	GTTTATGTCGGCTTAC	41	105	100	>200
91.000801	x	x	CIGCCATGGCTAAACCC	44	110	110	160
91.000801	x	x	TITTAGACATACAGGAGT	43	61	61	-
91.000801	x	x	CCCTTACCCACACCTT	35	75	>200	200
91.000803	x	x	CCCTTAAACCAACAGGAG	48	125	125	200
91.001212	x	x	TTATGATAGGAAAT	42	107	-	-
91.001212	x	x	TCTCTCTCTGAGTGTAA	46	100	100	-
91.001212	x	x	GAGGGCTCTAGGGCTT	50	72	72	>200
91.001212	x	x	TGGGAATGAGAAAATAC	46	83	83	20
91.001212	x	x	TACATACAGATGAGAGAGTC	44	80	80	-
91.001212	x	x	ATCTGCTCTCTGAGTGTAA	46	62	60	180
91.001212	x	x	AGGTATTTGCTCCTGTT	48	87	87	>200
91.001212	x	x	AGACACACATCAAGATG	46	90	90	200
91.001212	x	x	CTAGTAACTACGCTGCTG	44	61	61	200
91.001212	x	x	TCTCTCTCTCTCTCTC	49	120	120	170
91.001212	x	x	TGCCCTGGCTGCTGATA	43	95	95	200
91.001212	x	x	AGTACGAGGGAGGAGATA	44	92	92	-
91.001212	x	x	CCTGGTCACCTTCAC	46	75	72	160
91.001212	x	x	GCTGGTACCTACCTAC	46	110	110	170
91.001212	x	x	AACCTCTGGGACAAACAT	48	91	89	160

Fig. 10

Fig. 11

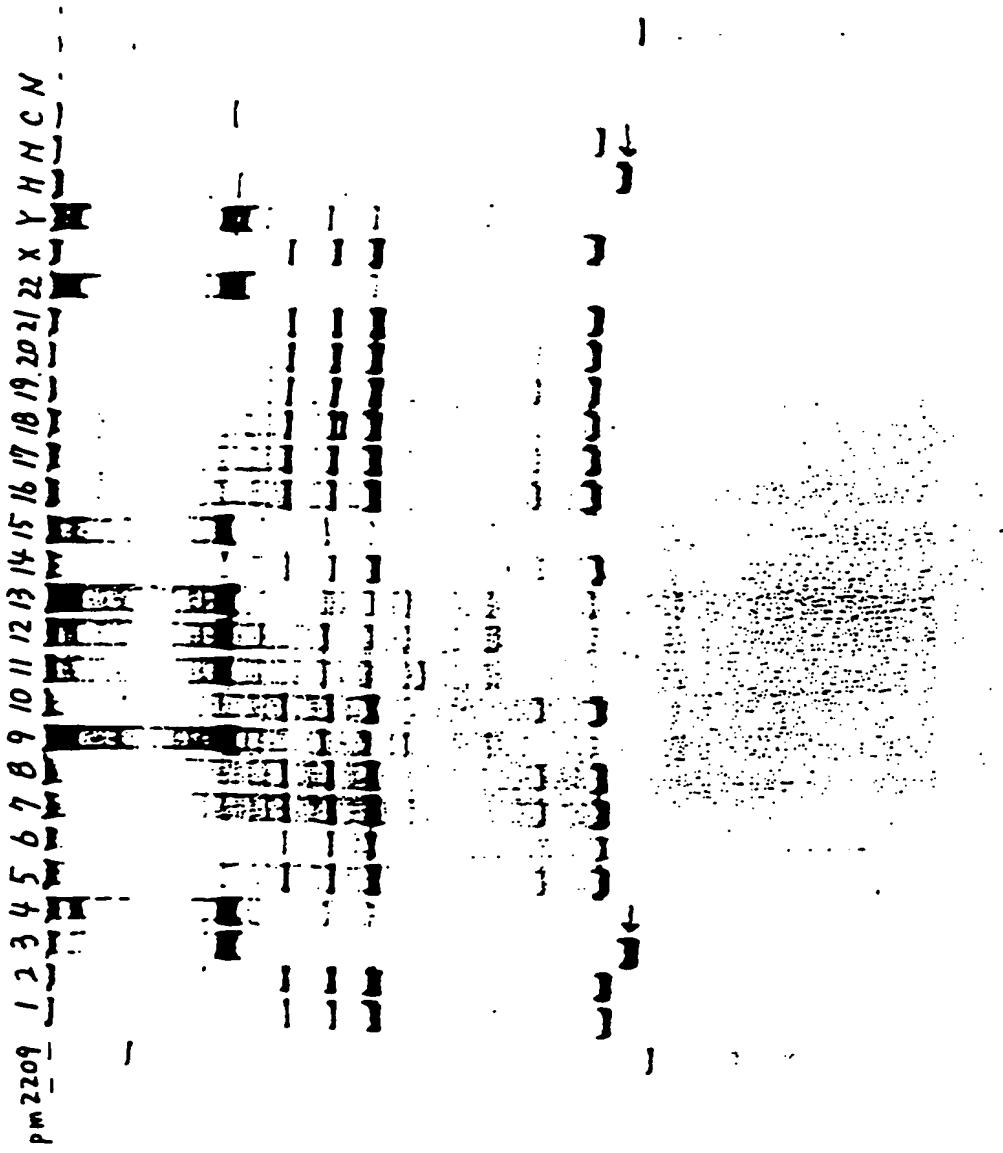


Fig. 12

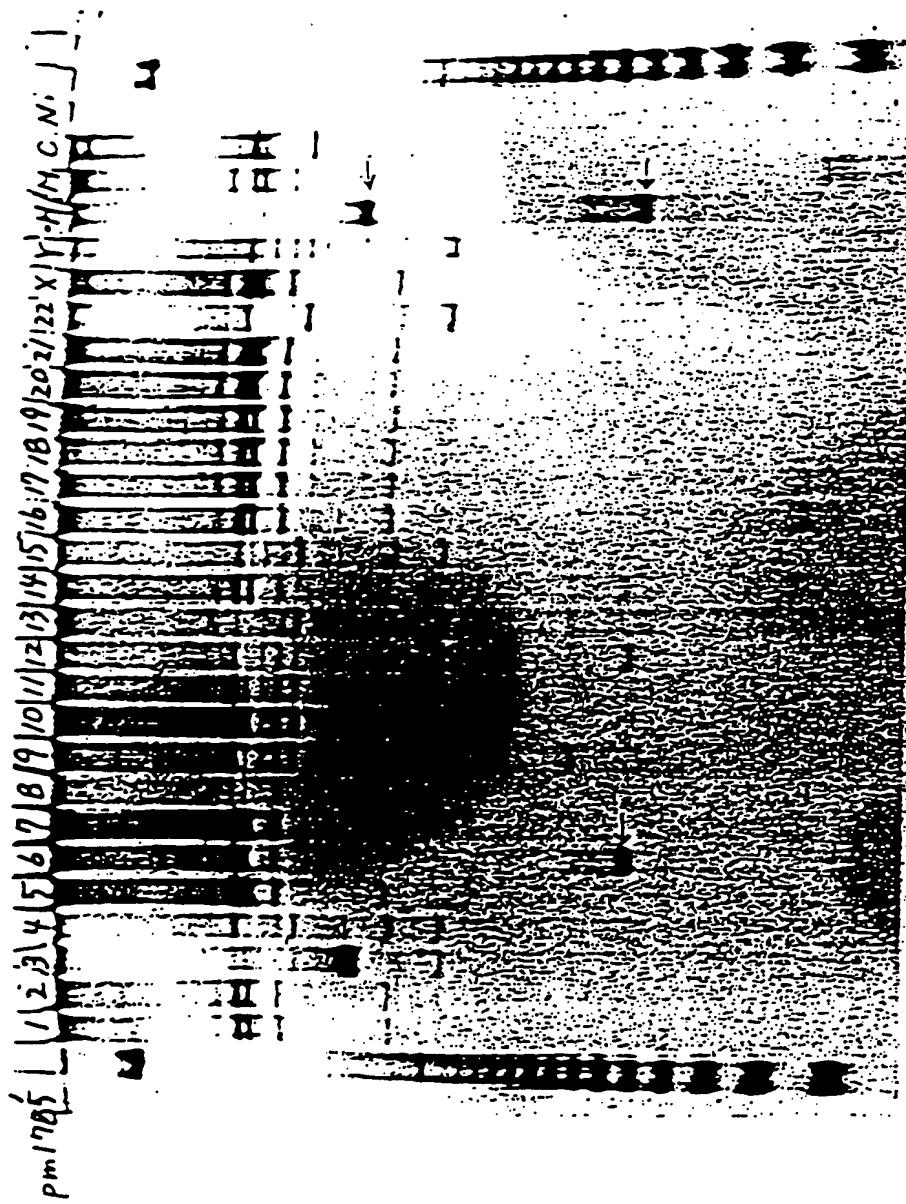


Fig. 13

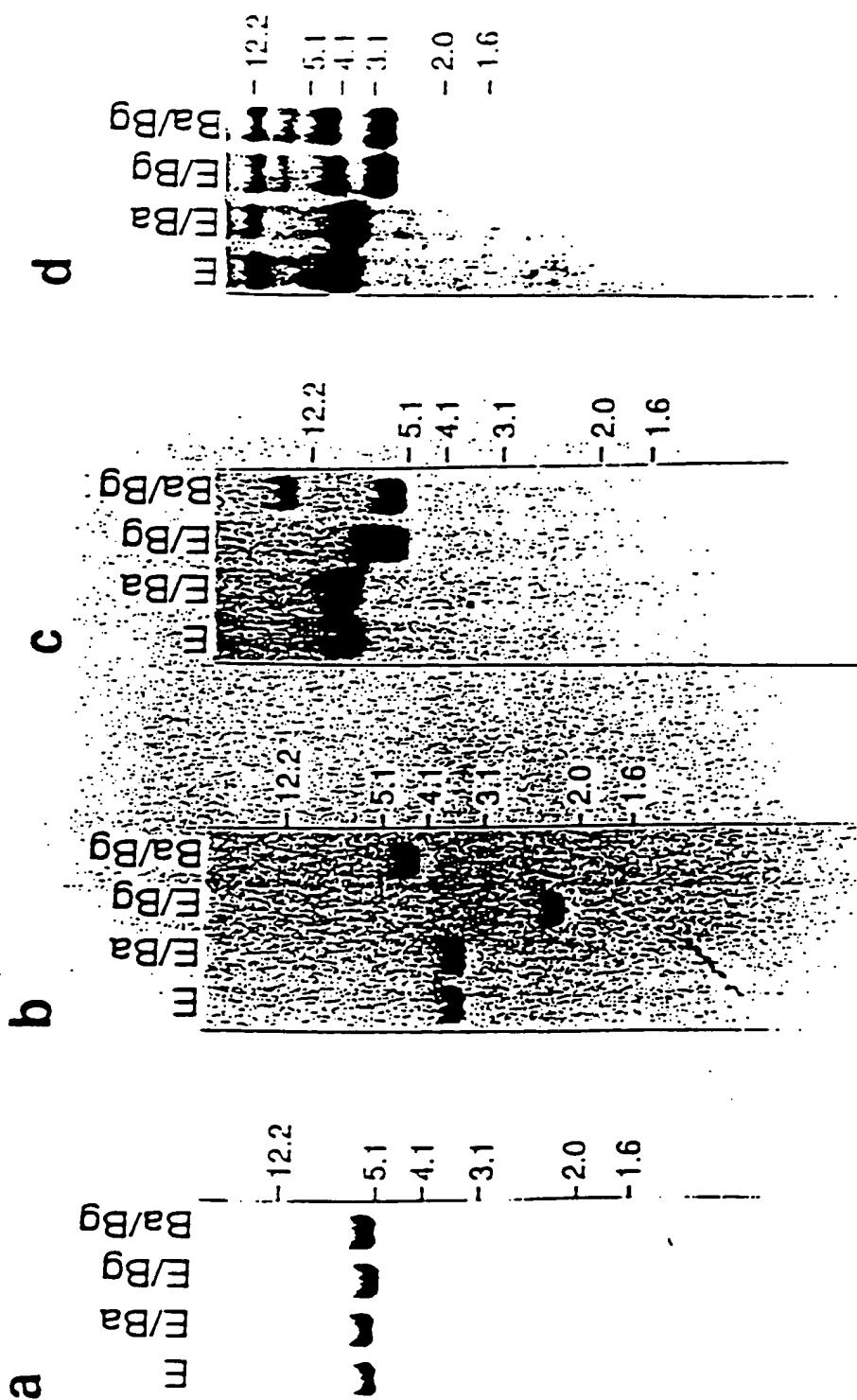


FIG. 14

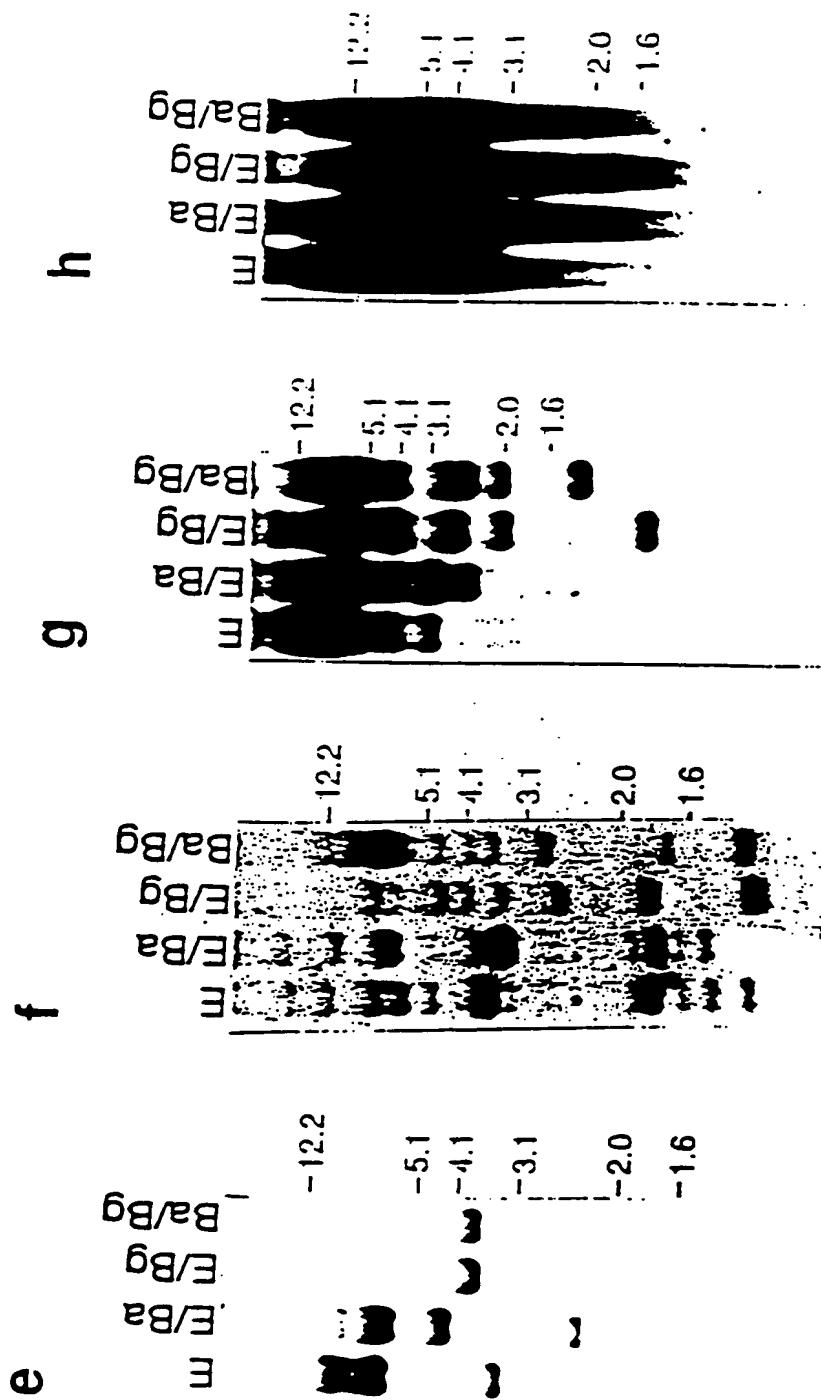


Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11416	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	61 (5)	17
GM03854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	61 (10)	0
GM06317	Y	CHW1103	91 (0)	9

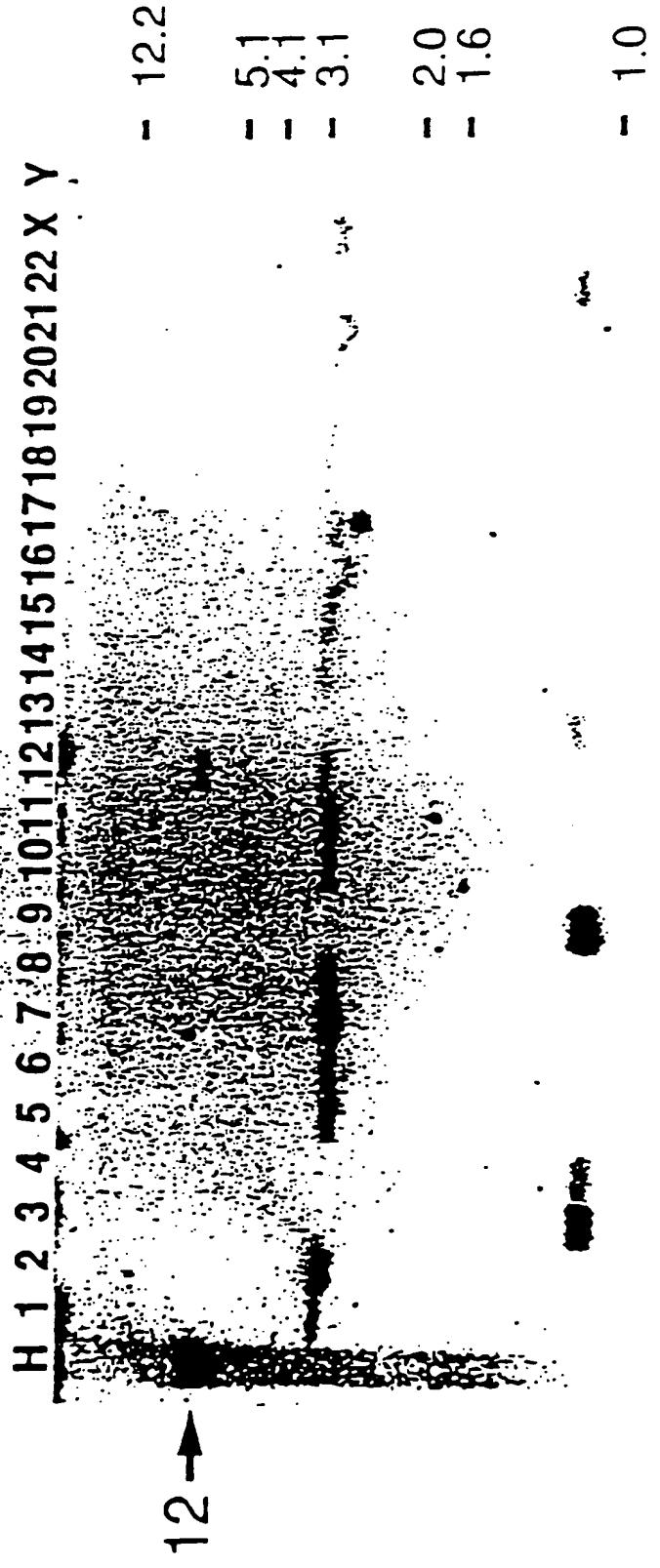
Fig. 16

a
Chromosome



Fig. 17

b
Chromosome



C

Chromosome

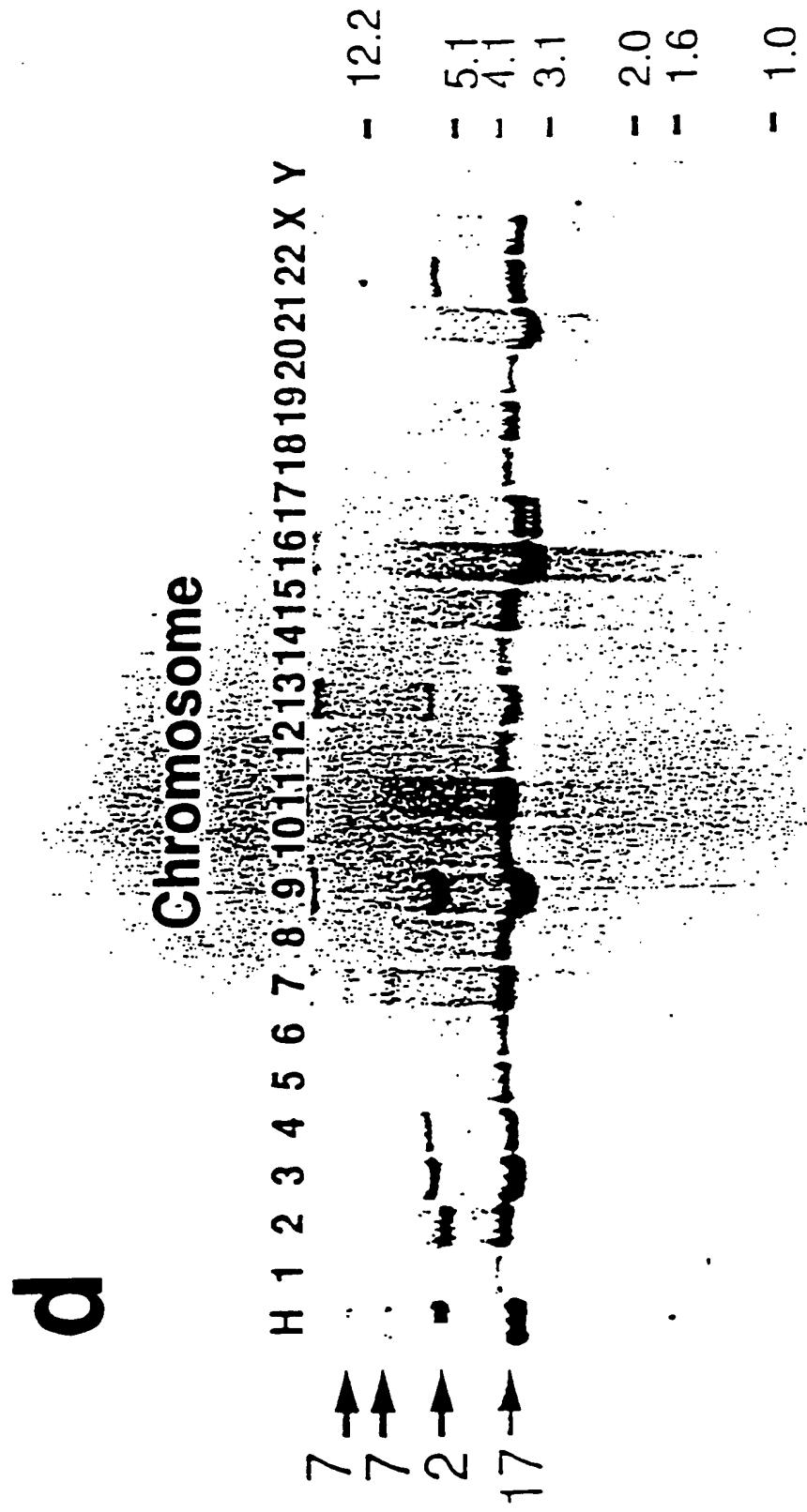
H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

23.1
9.4
6.6
4.4
2.3
2.0

2 →
1 →

Fig. 18

Fig. 19



EP 0 679 716 A1

Fig. 20

6

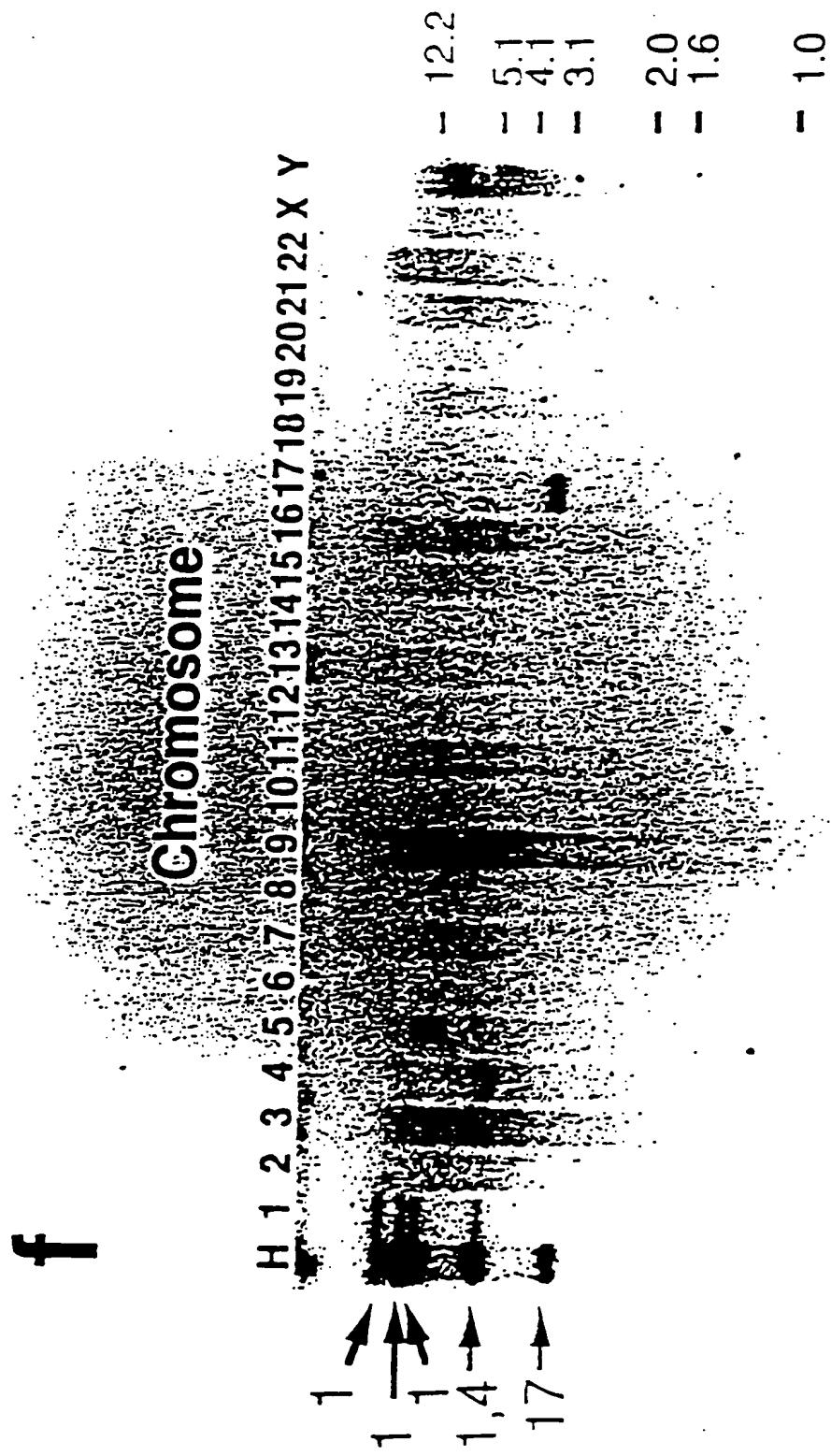
Chromosome

H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

7,19
8
11,12
11

- 12.2
- 5.1
- 4.1
- 3.1
- 2.0
- 1.6

Fig. 21



g

Chromosome



Fig. 22

Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes						Chromosomes assigned		Background	
Clone	Sequence length	3	3/3	3/3; 3+3			Mouse	Chinese hamster	
Single band group:									
e12e11	GS000073	432	1	1	1	1	9	0	0
e12e06	GS000062	540	1	1	1	1	6.15	0	0
e12g01	GS000290	212	1	1	1	1	2	1	1
e13e05	GS000117	359	1	1	1	1	11+	0	0
e13e07	GS000120	355	1	1	1	1	2	0	0
e13f10	GS000206	267	1	1	1	1	14	0	0
e13h01	GS000273	133	1	1	1	1	12+	0	0
e13h02	GS000322	167	1	1	1	1	6	0	0
e03g02	GS000095	397	1	1	1	1	3	0	0
e05h07	GS000154	313	1	1	1	1	11	1	1
e15e10	GS000343	151	1	1	1	1	20	0	0
hm01e12	GS000223	246	1	1	1	1	27	0	0
hm01e09	GS000423	157	0	1	1	1	1	0	0
hm01e12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000033	477	1	1	1	1	6	0	0
hm01h07	GS000015	363	1	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02e01	GS000293	271	1	1	1	1	15	0	0
hm02e01	GS000015	590	1	1	1	1	20	0	0
hm02e02	GS000342	156	0	1	1	1	14	0	0
hm02e05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g01	GS000191	273	1	1	1	1	17	0	0
hm05e05	GS000251	219	1	1	1	1	6	2	0
hm05e10	junk	392	1	1	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	1	0	0
km2d01	junk	169	1	1	1	0	n.d.	0	0
st10s	GS000001	703	1	1	1	1	5	0	0
st110	GS000057	471	1	1	1	1	3	0	0
st11d11	GS000307	#175	0	0	0	1	7	0	0
st11h01	GS000253	204	1	1	1	1	3	0	0
st147	GS000060	461	1	1	1	0	2	0	0
st14e06	junk	619	1	1	1	1	1	0	0
st14g02	GS000152	322	1	1	1	1	2	0	0
st14h12	GS000271	193	1	1	1	1	2	1	1
st150	GS000143	330	1	1	1	1	17	0	0
st156	GS000002	306	1	1	1	1	2	1	1
st15b11	GS000250	221	1	1	1	1	14	0	0
st179	GS000273	196	1	1	1	1	n.d.	0	0
st246	GS000224	241	1	1	1	1	9	0	0
st247	GS000347	153	1	1	1	1	1	0	0
st270	junk	135	1	1	1	1	19	0	0

Fig. 24

Clone	Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background	
	Sequence length	5	5/9 ₁	5/3 ₁	3/1/3 ₁			Chinese Mouse hamster	
s306	GSJ00256	205	1	1	0	1	X	0	0
s309	GSJ00171	105	1	1	0	1	1	0	0
s342	GSJ00323	165	1	1	1	1	4	3	2
s331	GSJ00255	207	1	1	0	1	6.15	1	1
s334	GSJ00163	312	1	1	1	1	1	0	0
s337	GSJ00276	195	1	1	1	1	17	0	0
s339	GSJ00295	130	1	1	1	1	n.d.	0	1
s443	GSJ00330	251	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GSJ00192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GSJ00334	161	1	1	1	1	14	1	1
s632	junk	337	1	1	1	1	2	2	1
s633	GSJ00163	311	1	1	1	1	22	2	1
s650	GSJ00041	644	1	1	1	1	12	1	1
tw1-04	GSJ00029	537	1	1	1	1	3.7	0	0
tw1-19	GSJ00218	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GSJ00237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-48	GSJ00093	178	1	1	1	1	14	0	0
tw1-96	GSJ00133	339	1	1	1	1	11	0	0
Two band group:									
s12212	GSJ00195	277	1	2	2	2	1.	1	1
s13d02	GSJ00042	503	2	2	1	1	2.	0	0
km01a06	GSJ00129	344	2	2	2	2	11.13	3	5
km01a07	GSJ000207	259	2	2	2	2	7.	0	0
km01d05	GSJ00232	243	2	2	2	1	2.	0	0
km01e01	GSJ00131	292	2	2	2	2	1.2	0	0
km02a08	GSJ00435	302	2	2	2	2	3.	1	1
km02c04	GSJ00221	253	2	2	2	2	3.	0	0
km02c05	GSJ00146	332	2	2	2	2	17,19,22	0	0
km03f07	GSJ00043	503	1	1	2	1	3.	0	0
s11d06	GSJ00268	205	2	2	2	2	11.12	0	0
s11g12	GSJ00037	255	2	2	2	2	6.	0	0
s124	GSJ00028	404	2	2	2	2	9.	1	1
s144	GSJ000132	342	1	2	2	2	1.7	0	0
s14f03	GSJ00029	243	1	2	2	2	2.	1	2
s15e02	junk	439	2	2	1	2	6.	0	0
s16b09	junk	420	1	1	1	2	10.14	0	0
s17c09	GSJ000248	223	2	2	2	2	14.	0	0
s231	junk	284	2	2	2	2	11.	0	0
s234	GSJ00124	193	2	2	2	2	1.	3	1
s235	GSJ00235	219	2	2	2	2	11.	0	0
s272	junk	195	2	2	2	2	10.16	1	1

Fig. 25

Clone	Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background	
	Sequence length	Σ	E/B_1	E/B_2	E/B_3	E/B_4		Mouse	Chinese hamster
s311	GSJ00092	333	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	GSJ00100	139	0	0	1	2	14,14	1	1
s336	GSJ00134	137	2	2	2	2	12,14	0	0
s333	GSJ00139	133	2	2	2	1	22.X	0	0
s339	GSJ00233	137	2	1	1	2	17.	0	0
s394	GSJ00063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GSJ00236	132	2	2	2	2	8,10	1	2
s465	GSJ00201	274	1	1	2	2	6,15	0	0
s635	junk	250	1	1	1	2	9,13	0	0
s639	GSJ00287	205	1	2	2	2	2X	0	0
s656	GSJ00025	590	2	2	0	2	6,11	0	0
tw1-33	junk	352	2	2	2	2	1.	0	0
tw1-39	GSJ00153	321	2	2	2	2	17.	0	0
tw1-70	GSJ00061	441	1	1	2	1	11.	0	0
tw1-80	junk	453	2	2	1	2	9,17	2	2
tw1-87	GSJ00158	316	2	2	2	2	7.	0	0
Three band group									
d0306	GSJ00080	417	3	3	3	1	1.	0	0
hm03b07	junk	336	2	3	3	3	5.	0	0.
hm03g02	GSJ00209	267	2	2	2	1	3,17,19	1	1
s129	GSJ000107	378	3	3	3	3	n.d.	1	1
s173	GSJ000257	146	1	2	2	3	2.	0	0
s17410	GSJ000294	131	3	3	3	3	2,13,22	1	1
s308	GSJ000412	633	2	2	2	3	XX	1	1
s401	GSJ000224	249	2	3	3	3	6,5.	0	0
s634	GSJ000045	491	3	3	3	3	1,22.	0	0
tw1-82	GSJ000208	267	3	3	3	3	13.	4	0
Four band group									
cl2g07	GSJ00154	320	4	4	2	3	5, 14.	0	0
cl3g08	GSJ00055	508	3	3	4	4	2,7,7,17	1	2
cl3e04	GSJ000106	#376	4	3	3	3	n.d.	0	2
cl3e09	GSJ000302	195	4	2	4	4	2,17.	7	2
s136	GSJ000160	315	4	4	4	4	4X	2	1
s163	GSJ000004	#613	4	4	4	2	4,4,8,20	1	1
s479	GSJ00130	293	4	4	2	2	7,3,11,11,12,19	0	0
Group with 5 or more bands									
cl2f08	GSJ00253	217	5	5	5	2	2,7,9,14.	2	0
hc01	junk	374	12	12	15	13	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
hc00	junk	173	6	2	3	3	6,3,9,19,21.	3	3
hm01e05	GSJ00205	176	9	7	5	5	X	9	8
hm01f04	GSJ00236	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Clone	Sequence length	Numbers of bands detected with human whole chromosomes					Chromosomes assigned		Background	
		3	3/3s	3/3q	3s/3q	Mouse	Chinese hamster			
hm02009	GS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0	
hm03102	GS000096	373	3	6	4	6	2,3,17,	3	3	
hm03104	GS000226	9239	6	6	6	7	a.d.	2	5	
km501	junk	350	3	3	3	3	13,	14	7	
s11f06	GS000319	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3	
s14f01	GS000407	252	12	11	10	9	1,4,9,13,	6	3	
s173	GS000094	397	5	4	6	3	1,1,1,4,17	0	0	
s255	GS000223	157	10	12	11	14	12,	9	5	
s341	junk	494	9	9	8	5	a.d.	15	3	
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1	
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X,	3	5	
tw1-63	junk	203	3	10	10	12	3,4,	17	11	
Bands no detected:										
el3g02	GS000340	157	0	0	0	0	-	-	-	
hm01e10	junk	232	0	0	0	0	-	-	-	
hm02d11	GS000274	196	0	0	0	0	-	-	-	
s323	GS000273	194	0	0	0	0	-	-	-	
s359	GS000199	279	0	0	0	0	-	-	-	
s511	junk	233	0	0	0	0	-	-	-	
s645	GS000012	0734	0	0	0	0	-	-	-	
s647	GS000105	360	0	0	0	0	-	-	-	
s651	junk	540	0	0	0	0	-	-	-	

INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER		
Int. Cl ⁶ C12N15/11, C12Q1/68//G01N33/566		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols)		
Int. Cl ⁶ C12N15/11, C12Q1/68//G01N33/566		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)		
BIOSIS PREVIEWS, CAS ONLINE		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA:coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed		
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search February 6, 1995 (06. 02. 95)		Date of mailing of the international search report March 7, 1995 (07. 03. 95)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.		Authorized officer Telephone No.

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International application No.

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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
X	Genes Dev., Vol. 7, 1993, Patton, J. G. et al. "Cloning and characterization of PSF a novel pre-mRNA splicing factor" p. 393-406	1-6 (706)
X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochim. Biophys. Acta., Vol. 1089, 1991, Tamura, T. et al. "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multicatalytic proteinase complexes)" p. 95-102	1-6 (775)
X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
X	Gene, Vol. 93, 1990 Taanman, J. W., Schrage, C., Ponne, N., Das, A., Bolhuis, P. A., de Vries, H. and Agsteribbe, E. Isolation of cDNAs encoding Subunit VIb of human cytochrome c oxidase and steady-state levels of coxVIb mRNA in different tissues p. 285-291	1-6 (844)
X	J. Biol. Chem., Vol. 264, 1989, Gray, P. W. et al. "Cloning of the cDNA of a human neutrophil bactericidal protein: Structural and functional correlations" p. 9505-9509	1-6 (861)
X	Immunogenetics, Vol. 32, 1990, Angelisova, P. et al. "The human leucocyte surface antigen CD53 is a protein structurally similar to the CD37 and MRC OX-44 antigens" p. 281-285	1-6 (1158)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Koken, M. H. et al. "Structural and functional conservation of two human homologs of the yeast DNA repair gene RAD6" p. 8865-8869	1-6 (1181)
X	Oncogene, Vol. 5, 1990, Fimmbach-Kraft, I. et al. "Tyk 2, prototype of a novel class of non-receptor tyrosine Kinase genes" p. 1329-1336	1-6 (1345)
X	Science, Vol. 248, 1990, Smith, C. A. et al. "A receptor for human tumor necrosis factor defines an unusual family of cellular and viral proteins" p. 1019-1023	1-6 (1431)

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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 263, 1988, Luster, A. D. et al. "Molecular and biochemical characterization of a novel gamma-interferon-inducible protein" p. 12036-12043	1-6 (1455)
X	J. Clin. Invest., Vol. 83, 1989, Look, A. T. et al. "The human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N" p. 1299-1307	1-6 (1469)
X	J. Cell Biol., Vol. 105, 1987, Argraves, W. S. et al. "Amino Acid Sequence of the Human Fibronectin Receptor" p. 1183-1190	1-6 (1607)
X	Nucleic Acids Res., Vol. 18, 1990, Liebhhaber, S. A. et al. "Characterization of a human cDNA encoding a widely expressed and highly conserved cysteine-rich protein with an unusual zinc-finger motif" p. 3871-3879	1-6 (1642)
X	J. Biol. Chem., Vol. 264, 1989, Didsbury, J. et al. "Rac, a novel ras-related family of proteins that are botulinum toxin substrates" p. 16378-16382	1-6 (1709)
X	EMBO J., Vol. 6, 1987, Willison, K. et al. "The human homologue of the mouse t-complex gene, TCP1, is located on chromosome 6 but is not near the HLA region" p. 1967-1974	1-6 (1749)
X	J. Biol. Chem., Vol. 266, 1991, Wu, Y. et al. "Activation of globin gene expression by cDNAs from induced K562 cells: Evidence for involvement of ferritin in globin gene expression" p. 17566-17572	1-6 (1785)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ikuta, T. et al "Three human alcohol dehydrogenase subunits: cDNA structure and molecular and evolutionary divergence" p. 634-638	1-6 (1864)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Fukumoto, H. et al "Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein" p. 5434-5438	1-6 (1878)

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Clin. Invest., Vol. 76, 1985, Cooke, N.E. et al. "Serum vitamin D-binding protein is a third member of the albumin and alpha fetoprotein gene family" p. 2420-2424	1-6 (1888)
X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
X	J. Biol. Chem., Vol. 266, 1991, Huang, S.-H. et al. "Additions and corrections Human deoxycytidine kinase. Sequence of cDNA clones and analysis of expression in cell lines with and without anzyme activity" p. 5353-5353	1-6 (1894)
X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al. "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
X	Gene, Vol. 44, 1986, Board, P. G. et al. "Molecular cloning and nucleotide sequence of human alpha-1 acid glycoprotein cDNA" p. 127-131	1-6 (1921)
X	Eur. J. Biochem., Vol. 155, 1986, Wathelet, M. et al. "Molecular cloning, full-length sequence and preliminary characterization of a 56-kDa protein induced by human interferons" p. 11-17	1-6 (2101)

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PCT/JP94/01916

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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids Res., Vol. 11, 1983, Chebath, J. et al. "Interferon induced 56,000 mr protein and its mRNA in human cells: molecular cloning and partial sequence of the cDNA" p. 1213-1226	1-6 (2101)
X	Biochemistry, Vol. 25, 1986, Koide, T. et al. "Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA" p. 2220-2225	1-6 (2174)
X	Biochemistry, Vol. 22, 1983, Friezner-Degen, S. J. et al. "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin" p. 2087-2097	1-6 (2214)
X	Biochem. J., Vol. 268, 1990, Steinkasserer, A. et al. "Heterogeneity in human serum amyloid A protein. Five different variants from one individual demonstrated by cDNA sequence analysis." p. 287-193	1-6 (2238)
X	Nucleic Acids Res., Vol. 17, 1989, Fabrizi, G. M. et al. "Sequence of a cDNA specifying subunit VIIa of human cytochrome c oxidase" p. 7107-7107	1-6 (2264)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 86, 1989, Sims, J. E. et al. "Cloning of the interleukin 1 receptor from human T cells" p. 8946-8950	1-6 (2265)
X	Eur. J. Biochem., Vol. 169, 1987, Mackinnon, C. M. et al. "Molecular cloning of cDNA for human complement component Cls. The complete amino acid sequence" p. 547-553	1-6 (2266)
X	J. Virol., Vol. 65, 1990, Tsujimoto, A. et al. "Isolation of cDNA for DNA binding proteins which specifically bind to TAX-responsive enhancer element in the LTR of HTLA-1" p. 1420-1426	1-6 (2475)
X	Immunogenetics, Vol. 37, 1993, Emi, N. et al. "Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfamily" p. 193-198	1-6 (2556)
X	Nature, Vol. 353, 1991, Kelly, A. P. et al. "A new human HLA class II-related locus, DM" p. 571-573	1-6 (2583)

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International application No.

PCT/JP94/01916

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Hla, T. et al. "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein-coupled receptors" p. 9308-9313	1-6 (2600)
X	J. Biol. Chem., Vol. 267, 1992, White, R. T. et al. "Human adipsin is identical to complement factor D and expressed at high levels in adipose tissue" p. 9210-9213	1-6 (2802)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Rouault, T. A. et al. "Cloning of the cDNA encoding RNA regulatory protein-the human iron-responsive element-binding protein" p. 7958-7962	1-6 (2832)
X	Nucleic Acids Res., Vol. 17, 1989, Sawada, R. et al. "Complementary DNA sequence and deduced peptide sequence for CD59/MEM43 antigen, the human homologue of murine lymphocyte antigen Ly-6c" p. 6728-6728	1-6 (2954)
X	DNA Cell Biol., Vol. 9, 1990, Sawada, R. et al. "Isolation and expression of the full-length cDNA encoding CD59 antigen of human lymphocytes" p. 213-220	1-6 (2954)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Weller, P. A. et al. "Complete sequence of human vinculin and assignment of the gene to chromosome 10" p. 5667-5671	1-6 (2983)
X	Cell, Vol. 58, 1989, Mellentin, J. D. et al. "LYL-1, a novel gene involved by chromosomal translocation in T-cell leukemia, codes for a protein with a helix-loop-helix DNA binding motif" p. 77-83	1-6 (3023)
X	Cell, Vol. 60, 1990, Uze, G. et al. "Genetic transfer of a functional human interferon alpha receptor into mouse cells: Cloning and expression of its cDNA" p. 225-234	1-6 (3041)
X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

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International application No.
PCT/JP94/01916

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
X	Nucleic Acids Res., Vol. 20, 1992, Wintzerith, M. et al. "Sequence of the human RNA polymerase II largest subunit" p. 910-910	1-6 (3083)
X	J. Cell Biol., Vol. 103, 1986, Lawler, J. et al. "The Structure of Human Thrombospondin, an/ adhesive Glycoprotein with Multiple Calcium binding Sites and Homologies with Several Different Proteins" p. 1635-1648	1-6 (3266)
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